

1. A method of interpreting data obtained from the analysis of nucleic acids, comprising the steps of:

transforming the nucleic acid data from the spatial domain to a frequency domain; and

2. A method according to Claim 1, wherein obtaining the nucleic acid data in the spatial domain comprises performing a gel electrophoresis process on nucleic acid material to form an image and performing a process on the image to obtain a machine-readable format of the image in the spatial domain.

3. A method according to Claim 2, further comprising performing a normalization process on the machine-readable image data prior to the transforming step.

4. A method according to Claim 2, wherein the spatial domain comprises size versus intensity.

5. A method according to Claim 1, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a Hadamard transform to obtain the nucleic acid data in the frequency domain.

6. A method according to Claim 1, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a Fourier transform to obtain the nucleic acid data in the frequency domain.

7. A method according to Claim 1, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a wavelet transform to obtain the nucleic acid data in the frequency domain.

8. A method according to any one of Claims 5 to 7, wherein the transformation results in frequency coefficients and the data mining process is performed utilizing the frequency coefficients.

9. A method according to Claim 8, wherein less than all of the frequency coefficients are used in the data mining process.

10. A method according to Claim 1, wherein the data mining process comprises processing the transformed data in a connectionist neural network algorithm.

11. A method according to Claim 1, wherein the data mining process comprises a feedforward, backpropagation connectionist algorithm.

12. A method according to any one of Claims 5 to 7, wherein the data mining process

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comprises a classification tree / rule induction (CART) algorithm.

13. An apparatus for interpreting data obtained by analysis of nucleic acids, comprising:

a memory that stores executable process steps; and

a processor that executes the executable process steps, wherein the executable process steps comprise (a) inputting nucleic acid data in a spatial domain, (b) transforming the nucleic acid data from the spatial domain to a frequency domain, and (c) obtaining sequence data of the nucleic acid data by executing a data mining process on the transformed nucleic acid data.

14. An apparatus according to Claim 13, wherein the input nucleic acid data is obtained by performing a gel electrophoresis process on nucleic acid material to form an image and performing a process on the image to obtain a machine-readable format of the image in the spatial domain.

15. An apparatus according to Claim 14, further comprising performing a normalization process on the machine-readable image data prior to the transforming step.

16. An apparatus according to Claim 14, wherein the spatial domain comprises size versus intensity.

17. An apparatus according to Claim 13, wherein the transforming step comprises subjecting

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the nucleic acid data in the spatial domain to a Hadamard transform to obtain the nucleic acid data in the frequency domain.

18. An apparatus according to Claim 13, wherein the transforming step comprises subjecting the nucleic data in the spatial domain to a Fourier transform to obtain the nucleic data in the frequency domain.

19. An apparatus according to Claim 13, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a wavelet transform to obtain the nucleic acid data in the frequency domain.

20. An apparatus according to any one of Claims 17 to 19, wherein the transformation results in frequency coefficients and the data mining process is performed utilizing the frequency coefficients.

21. An apparatus according to Claim 20, wherein less than all of the frequency coefficients are used in the data mining process.

22. An apparatus according to Claim 13, wherein the data mining process comprises processing the transformed data in a connectionist neural network algorithm.

23. An apparatus according to Claim 13, wherein the data mining process comprises a

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feedforward, backpropagation connectionist algorithm.

24. An apparatus according to any one of Claims 17 to 19, wherein the data mining process comprises a classification tree / rule induction (CART) algorithm.

25. Computer-executable process steps for interpreting data obtained by analysis of nucleic acids, the executable process steps comprising:

inputting nucleic acid data in a spatial domain;

transforming the input nucleic acid data from the spatial domain to a frequency domain; and

obtaining sequence data of the nucleic acid data by executing a data mining process on the transformed nucleic acid data.

26. Computer-executable process steps according to Claim 25, wherein the input nucleic acid data is obtained by performing a gel electrophoresis process on nucleic acid material to form an image and performing a process on the image to obtain a machine-readable format of the image in the spatial domain.

27. Computer-executable process steps according to Claim 26, further comprising performing a normalization process on the machine-readable image data prior to the transforming step.

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28. Computer-executable process steps according to Claim 26, wherein the spatial domain comprises size versus intensity.

29. Computer-executable process steps according to Claim 25, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a Hadamard transform to obtain the nucleic acid data in the frequency domain.

30. Computer-executable process steps according to Claim 25, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a Fourier transform to obtain the nucleic acid data in the frequency domain.

31. Computer-executable process steps according to Claim 25, wherein the transforming step comprises subjecting the nucleic acid data in the spatial domain to a wavelet transform to obtain the nucleic acid data in the frequency domain.

32. Computer-executable process steps according to any one of Claims 29 to 31, wherein the transformation results in frequency coefficients and the data mining process is performed utilizing the frequency coefficients.

33. Computer-executable process steps according to Claim 32, wherein less than all of the frequency coefficients are used in the data mining process.

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35. Computer-executable process steps according to Claim 25, wherein the data mining process comprises a feedforward, backpropagation connectionist algorithm.

37. A computer-readable medium which stores computer-executable process steps for interpreting data obtained by analysis of nucleic acids, the computer-executable process steps comprising:

transforming the input nucleic acid data from the spatial domain to a frequency domain; and obtaining sequence data of the nucleic acid data by executing a data mining process on the transformed nucleic acid data.

38. A computer-readable medium according to Claim 37, wherein the input nucleic acid data is obtained by performing a gel electrophoresis process on nucleic acid material to form an image and performing a process on the image to obtain a

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the data mining process is performed utilizing the frequency coefficients.

45. A computer-readable medium according to Claim 44, wherein less than all of the frequency coefficients are used in the data mining process.

46. A computer-readable medium according to Claim 37, wherein the data mining process comprises processing the transformed data in a connectionist neural network algorithm.

47. A computer-readable medium according to Claim 37, wherein the data mining process comprises a feedforward, backpropagation connectionist algorithm.

48. A computer-readable medium according to any one of Claims 41 to 43, wherein the data mining process comprises a classification tree/ rule induction (CART) algorithm.

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